

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 12, 2002, 20:42:35 ; Search time 23.96 seconds  
(without alignments)  
325.944 Million cell updates/sec

Title: US-09-525-867-1

Perfect score: 1118

Sequence: 1 MAVLSAPGLRGFRILGRSS.....ILOLQRIKRRRLQIWR 213

Scoring table:

BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1108	99.1	213	1 NUKM_HUMAN	075251 homo sapien
2	965.5	86.4	216	1 NUKM_BOVIN	P42026 bos taurus
3	736	65.8	215	1 NUKM_BRAOL	P42027 brassica ol
4	732.5	65.5	213	1 NUKM_SOLITU	Q43844 solanum tub
5	726.5	65.0	199	1 NUKM_CABEL	Q94360 caenorhabdi
6	725	64.8	218	1 NUKM_ARATH	Q42577 arabidopsis
7	719.5	64.4	226	1 NUKM_NEUCR	Q47950 neurospora
8	718	64.2	182	1 NUKM_RECAM	Q21272 recclinomona
9	654.5	58.5	174	1 NUKM_RICPR	Q32482 rickettsia
10	643	57.5	177	1 NUKM_RHOCA	Q84970 rhodobacter
11	639	57.2	192	1 NUKM_RHIME	Q68853 rhizobium m
12	626	56.0	173	1 NUKM_PARDE	P29918 paracoccus
13	561	50.2	156	1 NUKM_PARTE	P15602 paramecium
14	521	46.6	179	1 NUKM_AQUAE	Q67334 aquifex ae
15	519	46.4	202	1 NUKM_TRYBB	Q26783 trypanosoma
16	502.5	44.9	167	1 NUKM_RHIME	P56897 rhizobium m
17	457	40.9	181	1 NUKM_TETH	Q35218 thermus aqu
18	444	39.7	220	1 NUKM_ECOLI	P33598 escherichia
19	440.5	39.4	247	1 NUKM_MESVI	Q9mur0 mesostigma
20	438	39.2	248	1 NUKC_SYNY3	P19050 synecocyst
21	437.5	39.1	184	1 NUKM_MYCTU	P95180 mycobacteri
22	431.5	38.6	225	1 NUKC_ARATH	P56756 arabidopsis
23	431.5	38.6	247	1 NUKC_TOBAC	Q06409 nicotiana t
24	429.5	38.4	244	1 NUKC_SPTOL	Q93m30 spinacia ol
25	429.5	38.4	245	1 NUKC_ANASQ	Q9xb17 anabaena sp
26	428	38.3	224	1 NUKM_BUCAI	P57253 buchnera ap
27	427.5	38.2	246	1 NUKC_ORYSA	P12159 oryza sativ
28	426.5	38.1	243	1 NUKC_MARPO	P06410 marchantia
29	424.5	38.0	219	1 NUKC_SYNY3	P17062 synecocyst
30	424	37.9	224	1 NUKM_ERWCA	O85274 erwinia car
31	423.5	37.9	226	1 NUKC_LUPLU	P52766 lupinus lut
32	423.5	37.9	245	1 NUKC_WHEAT	P26304 triticum ae
33	422.5	37.8	248	1 NUKC_MAIZE	P06670 zea mays (m

34	420.5	37.6	245	1 NUKC_ANASP	Q44240 anabaena sp
35	408.5	36.5	224	1 NUKC_SOYBN	P31175 glycine max
36	275	24.6	255	1 HYFL_ECOLI	P16433 escherichia
37	255	22.8	252	1 HYFL_ECOLI	P77668 escherichia
38	131	11.7	80	1 NUKC_ANTFO	Q31791 anthoceros
39	104	9.3	230	1 FRHG_METJA	Q60340 methanococ
40	97.5	8.7	235	1 FRHG_METTH	P19498 methanobact
41	97	8.7	216	1 Y736_METJA	Q58136 methanococ
42	92.5	8.3	1239	1 V120_EBV	P03189 Epstein-Bar
43	88.5	7.9	510	1 PNTA_ECOLI	Q07001 escherichia
44	82	7.3	243	1 FRHG_METVO	Q00393 methanococ
45	80	7.2	209	1 HOXY_ALCEU	P22319 alcalligenes

## ALIGNMENTS

RESULT	1
NUKM_HUMAN	
ID	NUKM_HUMAN
AC	075251
DT	15-JUL-1999 (Rel. 38, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DE	20-AUG-2001 (Rel. 40, Last annotation update)
DE	NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT, MITOCHONDRIAL PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT).
GN	NDUFS7
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97092888; PubMed=8938450;
RA	Hyslop S.J., Duncan A.M., Pitkanen S., Robinson B.H.;
RT	"Assignment of the PSST subunit gene of human mitochondrial complex I to chromosome 19p13."
RL	Genomics 37:375-380(1996).
RN	[2]
RP	SEQUENCE OF 56-213 FROM N.A.
RA	Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA	Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA	Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA	Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
RA	Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA	Krommiller B., Arellano A., Montgomey M., Ow D., Nolan M., Trong S.,
RA	Kobayashi A., Olsen A.S., Carrano A.V.;
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	VARIANT LS MET-122.
RX	MEDLINE=99287516; PubMed=10360771;
RA	Triepels R.H., van den Heuvel L., Loeffen J.L., Buskens C.A.,
RA	Smeets R.J., Rubio Gozalbo M.E., Budde S.M., Mariman E.C.,
RA	Wijburg F.A., Barth P.G., Trijbels J.M.F., Smeitink J.A.;
RT	"Leigh syndrome associated with a mutation in the NDUFS7 (PSST) nuclear encoded subunit of complex I";
RL	Ann. Neurol. 45:787-790(1999)
CC	-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
CC	-1- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
CC	-1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
CC	-1- DISEASE: DEFECTS IN NDUFS7 ARE A CAUSE OF LEIGH SYNDROME (LS); A SEVERE NEUROLOGICAL DISORDER CHARACTERIZED BY BILATERALLY SYMMETRICAL NECROTIC LESIONS IN SUBCORTICAL BRAIN REGIONS.
CC	-1- SIMILARITY: BELONGS TO THE COMPLEX I 20 KDA SUBUNIT FAMILY.

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EMBL: AC005329; AAC27669.1; -  
 DR MM: 601825; -  
 DR MM: 256000; -  
 DR InterPro: IPR002096; Complex1\_20kD.  
 DR Pfam: PF01058; oxidored\_g6; 2.  
 DR PROSITE: PS01150; COMPLEX1\_20K; 1.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;  
 FT TRANSIT 1 38  
 FT CHAIN 39 213  
 FT METAL 88 88  
 FT METAL 89 89  
 FT METAL 153 153  
 FT METAL 183 183  
 FT VARIANT 122 122  
 FT V -> M (IN LS).  
 FT /FTID=VAR-008848.  
 FT SEQUENCE 213 AA: 23579 MW; B863199E06538DEC CRC64;  
 Query Match 99.1%; Score 1108; DB 1; Length 213;  
 Best Local Similarity 99.5%; Pred. No. 2.8e-99;  
 Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAVLSAPGLRGFRILGLRSSVGPVAVQARGVHQSVDTPGSPSTQPALPKARAVAPKPSRRG 60  
 DB 1 MAVLSAPGLRGFRILGLRSSVGLAVQARGVHQSVDTPGSPSTQPALPKARAVAPKPSRRG 60  
 QY 61 EYVAKLDLVNWRSSLSLWPTFTGLACCAVEMHMAAPRYDMDRFGVFRASPRQSDVM 120  
 DB 61 EYVAKLDLVNWRSSLSLWPTFTGLACCAVEMHMAAPRYDMDRFGVFRASPRQSDVM 120  
 QY 121 IVAGILTNNKMAPALRKVYDQMPPEPRYVYVSMGSCANGGYYHYYSVVRGCDRIVPVDIYI 180  
 DB 121 IVAGILTNNKMAPALRKVYDQMPPEPRYVYVSMGSCANGGYYHYYSVVRGCDRIVPVDIYI 180  
 QY 181 PGCPPTAEALLYGILQLOKRIKRRRLQIWR 213  
 DB 181 PGCPPTAEALLYGILQLOKRIKRRRLQIWR 213

RESULT 2  
 NUKM\_BOVIN  
 ID NUKM\_BOVIN STANDARD; PRT; 216 AA.  
 AC P42026;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT, MITOCHONDRIAL PRECURSOR  
 DE (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT).  
 GN NDUF57.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=9249573; PubMed=1577158;  
 RA Arizemendi J.M., Runswick M.J., Skehel J.M., Walker J.E.;  
 RT "NADH: ubiquinone oxidoreductase from bovine heart mitochondria. A  
 FT fourth nuclear encoded subunit with a homologue encoded in  
 FT chloroplast genomes";  
 RL FEBS Lett. 301:237-242(1992).  
 CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.  
 CC -|- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.  
 CC -|- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.  
 CC -|- SIMILARITY: BELONGS TO THE COMPLEX I 20 KDA SUBUNIT FAMILY.  
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 CC or send an email to license@isb-sib.ch).

CC EMBL: X65020; CAA46154.1;  
 DR InterPro: IPR002096; Complex1\_20kD.  
 DR Pfam: PF01058; oxidored\_g6; 1.  
 DR PROSITE: PS01150; COMPLEX1\_20K; 1.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;  
 FT TRANSIT 1 37  
 FT CHAIN 38 216  
 FT METAL 91 91  
 FT METAL 92 92  
 FT METAL 156 156  
 FT METAL 186 186  
 FT SEQUENCE 216 AA: 23771 MW; 514B8A63C59BE641 CRC64;  
 Query Match 86.4%; Score 965.5; DB 1; Length 216;  
 Best Local Similarity 85.7%; Pred. No. 1.4e-85;  
 Matches 186; Conservative 11; Mismatches 15; Indels 5; Gaps 2;  
 QY 1 MAVLSAPGLRGFRILGLRSSVGPVAVQARGVHQSVDTPGSPSTQPALPKARAVAPKPSRRG 56  
 DB 1 MAALAARLL-L-HPTLAVRSGVGAALQVRGVHSSMAADSPSTQPAVSQARAVVPKPAALP 59  
 QY 57 SSRGEYVYVAKLDLVNWRSSLSLWPTFTGLACCAVEMHMAAPRYDMDRFGVFRASPRQ 116  
 DB 60 SSRGEYVYVAKLDLVNWRSSLSLWPTFTGLACCAVEMHMAAPRYDMDRFGVFRASPRQ 119  
 QY 117 SDVMIVAGILTNNKMAPALRKVYDQMPPEPRYVYVSMGSCANGGYYHYYSVVRGCDRIVP 176  
 DB 120 SDVMIVAGILTNNKMAPALRKVYDQMPPEPRYVYVSMGSCANGGYYHYYSVVRGCDRIVP 179  
 QY 177 DIVPGCPPTAEALLYGILQLOKRIKRRRLQIWR 213  
 DB 180 DIVPGCPPTAEALLYGILQLOKRIKRRRLQIWR 216

RESULT 3  
 NUKM\_BRAOL  
 ID NUKM\_BRAOL STANDARD; PRT; 215 AA.  
 AC P42027;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT, MITOCHONDRIAL PRECURSOR  
 DE (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD).  
 OS Brassica oleracea (Cauliflower).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OC NCBI\_TaxID=3712;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. SHOGUN; TISSUE=Flowers;  
 RX MEDLINE=95334517; PubMed=7610188;  
 RA Pogson B.J., Downs C.G., Davies K.M., Morris S.C.,  
 RA Buchanan-Wollaston V.;  
 RT "Nucleotide sequence of a cDNA clone from broccoli with high identity  
 RT with the PSST subunit of NADH:ubiquinone oxidoreductase";  
 RL Plant Physiol. 108:859-860(1995).  
 CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.  
 CC -|- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.  
 CC -|- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.  
 CC -|- SIMILARITY: BELONGS TO THE COMPLEX I 20 KDA SUBUNIT FAMILY.  
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